

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC	ATG GAT CCG GCG GCG	55
	Met Asp Pro Ala Ala	
	1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC	103	
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala		
10 15 20		
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG	151	
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu		
25 30 35		
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG	199	
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met		
40 45 50		
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG	247	
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu		
55 60 65		
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT	295	
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala		
70 75 80 85		
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343	
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly		
90 95 100		
GCG CGG CTG GAC GTG GCG GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391	
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu		
105 110 115		
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439	
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala		
120 125 130		
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487	

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Sub-I

Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
135 140 145

GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT 538
Gly Pro Ser Asp Ile Pro Asp
150 155

CGGGAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACCTGC CCCTGCCACA 598

ACCCACCCCG CTTTCGTAGT TTTCATTTAG AAAATAGAGC TTTTAAAAAT GTCCTGCCTT 658

TTAACGTAGA TATAAGCCTT CCCCCACTAC CGTAAATGTC CATTATATC ATTTTTTATA 718

TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTTCACT GTGTTGGAGT 778

TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTC TTGCGAGCCT 838

CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAACCTAGG GAAGCTCAGG 898

GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA 958

AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA 994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30

Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
50 55 60

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65 70 75 80

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
85 90 95

Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100 105 110

Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115 120 125

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Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130 135 140

Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG 60
CGCTAGGCGC TTTTTCCTCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGGCCACGGA 120
AAAGCCCCTGA GCTAACGACC GGCCGCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA 180
GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCGG 240
AGCAGCGTGG GAAAGAAGGG AAGAGTGTCG TTAAGTTTAC GGCCAACGGT GGATTATCCG 300
GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG 351
Met Arg Glu Glu Asn Lys Gly Met
1 5
CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399
Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
10 15 20
CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447
Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
25 30 35 40
GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495
Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
45 50 55
AGC GCC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543
Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn
60 65 70
TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591
Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg

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75	80	85	
GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG			639
Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg			
90	95	100	
CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG			687
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu			
105	110	115	120
GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG			735
Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly			
125	130	135	
GAC TGACGCCAGG TTCCCCAGCC GCCCACAACG ACTTTATTTT CTTACCCAAT			788
Asp			
TTCCCACCCC CACCCACCTA ATTCGATGAA GGCTGCCAAC GGGGAGCGG			837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu			
1	5	10	15
Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser			
20	25	30	
Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg			
35	40	45	
Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu			
50	55	60	
Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr			
65	70	75	80
Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val			
85	90	95	
Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly			
100	105	110	
Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala			
115	120	125	
Gly Tyr Leu Arg Thr Ala Thr Gly Asp			

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130

135

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC	60
GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG	120
GACAGCGAGC TGCCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG	180
AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC	233
Met Met Met Gly Asn Val His	
1 5	
GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC	281
Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp	
10 15 20	
CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC	329
Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe	
25 30 35	
CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG	377
Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val	
40 45 50 55	
CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA	425
Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly	
60 65 70	
CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT	473
His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys	
75 80 85	
TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC	521
Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp	
90 95 100	
GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC	569
Gly His Ser Phe Ser Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly	
105 110 115	

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CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT 617
Gln Ser Gln Glu Gln Ser
120 125

TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA 677

TGCTTTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA 737

GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCGCGAAGG 797

GAATAATGGC TGGATTGTTT AAAAAAATAA AATAAAGATA CTTTTTAAAA TGTCAA 853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
1 5 10 15

Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His
20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
35 40 45

Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
50 55 60

Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
65 70 75 80

Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
85 90 95

Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro
100 105 110

Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

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Ala	Leu	Leu	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Ala	Leu	Asn	Arg	Phe	Gly
1				5					10					15	
Arg	Arg	Pro	Ile	Gln	Val	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu
			20					25					30		
Leu	Leu	Leu	Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr
			35				40					45			
Leu	Thr	Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr
	50					55					60				
Leu	Val	Val	Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val			
65				70						75					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15
Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
20 25 30
Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
35 40 45
Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60
Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80
Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95
Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110
Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125
Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140
Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160
Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175
Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190
Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205
Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
210 215 220
Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg

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(2) INFORMATION FOR SEQ ID NO:10:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Glu	Lys	Asp	Gly	Leu	Cys	Arg	Ala	Asp	Gln	Gln	Tyr	Glu	Cys	Val
1				5					10					15	
Ala	Glu	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Lys	Val	Phe	Lys	Ala	Xaa	Asp
			20					25					30		
Leu	Lys	Asn	Gly	Gly	Arg	Phe	Val	Ala	Leu	Lys	Arg	Val	Arg	Val	Gln
		35					40					45			
Thr	Gly	Glu	Gln	Gly	Met	Pro	Leu	Ser	Thr	Ile	Arg	Glu	Val	Ala	Val
	50					55					60				
Leu	Arg	His	Leu	Glu	Thr	Phe	Glu	His	Pro	Asn	Val	Val	Arg	Leu	Phe
65					70					75					80
Asp	Val	Cys	Thr	Val	Ser	Arg	Thr	Asp	Arg	Glu	Thr	Lys	Leu	Thr	Leu
				85					90					95	
Val	Phe	Glu	His	Val	Asp	Gln	Asp	Leu	Thr	Thr	Tyr	Leu	Asp	Lys	Val
			100					105					110		
Pro	Glu	Pro	Gly	Val	Pro	Thr	Glu	Thr	Ile	Lys	Asp	Met	Met	Phe	Gln
		115					120					125			
Leu	Leu	Arg	Gly	Leu	Asp	Phe	Leu	His	Ser	His	Arg	Val	Val	His	Arg
		130				135					140				
Asp	Leu	Lys	Pro	Gln	Asn	Ile	Leu	Val	Thr	Ser	Ser	Gly	Gln	Ile	Lys
145					150					155					160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu
165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu
180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile
195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp
210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu
225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser
245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu
260 265 270

Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg
275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu
290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr
305 310 315 320

Ser Glu Leu Asn Thr Ala
325

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